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Pu/09/1/2/02

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/719,748

DATE: 06/12/2001

TIME: 11:47:46

Input Set : A:\KIMCHI2A.txt

Output Set: N:\CRF3\06122001\I719748.raw

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 JAN 29 2002
 TECH CENTER 1600/2900**

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3 <110> APPLICANT: KIMCHI, Adi
5 <120> TITLE OF INVENTION: DAP-KINASE RELATED PROTEIN
7 <130> FILE REFERENCE: KIMCHI2A
9 <140> CURRENT APPLICATION NUMBER: 09/719,748
10 <141> CURRENT FILING DATE: 2000-12-15
12 <150> PRIOR APPLICATION NUMBER: 60/089,294
13 <151> PRIOR FILING DATE: 1998-06-15
15 <160> NUMBER OF SEQ ID NOS: 14
17 <170> SOFTWARE: PatentIn Ver. 2.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1742
21 <212> TYPE: DNA
22 <213> ORGANISM: Human
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (62)..(1141)
28 <400> SEQUENCE: 1
29 gaccgcggca gctcagcctc ccgcccattg tatgttccag gcctcaatga ggagtccaaa 60
31 c atg gag cca ttc aag cag cag aag gtg gag gac ttt tat gac atc gga 109
32 Met Glu Pro Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile Gly.
33 1 5 10 15
35 gag gag ctg ggg agt ggc cag ttt gcc atc gtg aag aag tgc cgg gag 157
36 Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg Glu
37 20 25 30
39 aag agc acg ggg ctt gag tat gca gcc aag ttc atc aag aag cgg cag 205
40 Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Gln
41 35 40 45
43 agc cgg gcg agc cgg cgc ggt gtg agc cgg gag gag atc gag cgg gag 253
44 Ser Arg Ala Ser Arg Arg Gly Val Ser Arg Glu Glu Ile Glu Arg Glu
45 50 55 60
47 gtg agc atc ctg cgg cag gtg ctg cac cac aat gtc atc acg ctg cac 301
48 Val Ser Ile Leu Arg Gln Val Leu His His Asn Val Ile Thr Leu His
49 65 70 75 80
51 gac gtc tat gag aac cgc acc gac gtg gtg cac atc ctt gag cta gtg 349
52 Asp Val Tyr Glu Asn Arg Thr Asp Val Val His Ile Leu Glu Leu Val
53 85 90 95
55 tct gga gga gag ctc ttc gat ttc ctg gcc cag aag gag tca ctg agt 397
56 Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu Ser
57 100 105 110
59 gag gag gag gcc acc agc ttc att aag cag atc ctg gat ggg gtg aac 445
60 Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val Asn
61 115 120 125
63 tac ctt cac aca aag aaa att gct cac ttt gat ctc aag cca gaa aac 493
64 Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu Asn
65 130 135 140
67 att atg ttg tta gac aag aat att ccc att cca cac atc aag ctg att 541
68 Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu Ile
    
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69 145          150          155          160
71 gac ttt ggt ctg gct cac gaa ata gaa gat gga gtt gaa ttt aag aat 589
72 Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys Asn
73          165          170          175
75 att ttt ggg acg ccg gaa ttt gtt gct cca gaa att gtg aac tac gag 637
76 Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu
77          180          185          190
79 ccc ctg ggt ctg gag gct gac atg tgg agc ata ggc gtc atc acc tac 685
80 Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr
81          195          200          205
83 atc ctc tta agt gga gca tcc cct ttc ctg gga gac acg aag cag gaa 733
84 Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln Glu
85          210          215          220
87 aca ctg gca aat atc aca tca gtg agt tac gac ttt gat gag gaa ttc 781
88 Thr Leu Ala Asn Ile Thr Ser Val Ser Tyr Asp Phe Asp Glu Glu Phe
89 225          230          235          240
91 ttc agc cat acg agc gag ctg gcc aag gac ttt att cgg aag ctt ctg 829
92 Phe Ser His Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu Leu
93          245          250          255
95 gtt aaa gag acc cgg aaa cgg ctc aca atc caa gag gct ctc aga cac 877
96 Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg His
97          260          265          270
99 ccc tgg atc acg ccg gtg gac aac cag caa gcc atg gtg cga cgg gag 925
100 Pro Trp Ile Thr Pro Val Asp Asn Gln Gln Ala Met Val Arg Arg Glu
101          275          280          285
103 tct gtg gtc aat ctg gag aac ttc agg aag cag tat gtc cgc agg cgg 973
104 Ser Val Val Asn Leu Glu Asn Phe Arg Lys Gln Tyr Val Arg Arg Arg
105          290          295          300
107 tgg aag ctt tcc ttc agc atc gtg tcc ctg tgc aac cac ctc acc cgc 1021
108 Trp Lys Leu Ser Phe Ser Ile Val Ser Leu Cys Asn His Leu Thr Arg
109 305          310          315          320
111 tcg ctg atg aag aag gtg cac ctg agg ccg gat gag gac ctg agg aac 1069
112 Ser Leu Met Lys Lys Val His Leu Arg Pro Asp Glu Asp Leu Arg Asn
113          325          330          335
117 tgt gag agt gac act gag gag gac atc gcc agg agg aaa gcc ctc cac 1117
118 Cys Glu Ser Asp Thr Glu Glu Asp Ile Ala Arg Arg Lys Ala Leu His
119          340          345          350
121 cca cgg agg agg agc agc acc tcc taactggcct gacctgcagt ggccgccagg 1171
122 Pro Arg Arg Arg Ser Ser Thr Ser
123          355          360
125 gaggttttggg cccagcgggg ctccttcttg tgcagacttt tggaccagc tcagcaccag 1231
127 caccggggcg tcctgagcac ttgtcaagag agatggggccc aagggaattca gaagagcttg 1291
129 caggcaagcc aggagaccct gggagctgtg gctgtcttct gtggaggagg ctccagcatt 1351
131 cccaaagctc ttaattctcc ataaaatggg ctttctcttg tctgccatcc tcagagtctg 1411
133 ggggtgggagt gtggacttag gaaaacaata taaaggacat cctcatcatc acggggtgaa 1471
135 ggtcagagta aggcagcctt cttcacaggc tgaggggggtt cagaaccagc ctggccaaaa 1531
137 attacaccag agagacagag tcctcccatc tgggaacagg gtgattgagg aaagtgaacc 1591
139 ttgggtgtga gggaccaatc ctgtgacctc ccagaacatc ggaagccagg acgtcaggct 1651
141 gaccaacacc tcagaccttc tgaagcagcc cattgctggc ccgccatgtt gtaattttgc 1711

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143 tcatttttat taaacttctg gtttacctga a 1742
146 <210> SEQ ID NO: 2
147 <211> LENGTH: 360
148 <212> TYPE: PRT
149 <213> ORGANISM: Human
151 <400> SEQUENCE: 2
152 Met Glu Pro Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile Gly
153 1 5 10 15
155 Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg Glu
156 20 25 30
158 Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Gln
159 35 40 45
161 Ser Arg Ala Ser Arg Arg Gly Val Ser Arg Glu Glu Ile Glu Arg Glu
162 50 55 60
164 Val Ser Ile Leu Arg Gln Val Leu His His Asn Val Ile Thr Leu His
165 65 70 75 80
167 Asp Val Tyr Glu Asn Arg Thr Asp Val Val His Ile Leu Glu Leu Val
168 85 90 95
170 Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu Ser
171 100 105 110
173 Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val Asn
174 115 120 125
176 Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu Asn
177 130 135 140
179 Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu Ile
180 145 150 155 160
182 Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys Asn
183 165 170 175
185 Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu
186 180 185 190
188 Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr
189 195 200 205
191 Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln Glu
192 210 215 220
194 Thr Leu Ala Asn Ile Thr Ser Val Ser Tyr Asp Phe Asp Glu Glu Phe
195 225 230 235 240
197 Phe Ser His Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu Leu
198 245 250 255
200 Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg His
201 260 265 270
203 Pro Trp Ile Thr Pro Val Asp Asn Gln Gln Ala Met Val Arg Arg Glu
204 275 280 285
206 Ser Val Val Asn Leu Glu Asn Phe Arg Lys Gln Tyr Val Arg Arg Arg
207 290 295 300
209 Trp Lys Leu Ser Phe Ser Ile Val Ser Leu Cys Asn His Leu Thr Arg
210 305 310 315 320
212 Ser Leu Met Lys Lys Val His Leu Arg Pro Asp Glu Asp Leu Arg Asn
213 325 330 335
215 Cys Glu Ser Asp Thr Glu Glu Asp Ile Ala Arg Arg Lys Ala Leu His

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216          340          345          350
218 Pro Arg Arg Arg Ser Ser Thr Ser
219          355          360
222 <210> SEQ ID NO: 3
223 <211> LENGTH: 263
224 <212> TYPE: PRT
225 <213> ORGANISM: Human
227 <400> SEQUENCE: 3
228 Tyr Asp Thr Gly Glu Glu Leu Gly Ser Gly Gln Phe Ala Val Val Lys
229   1          5          10          15
231 Lys Cys Arg Glu Lys Ser Thr Gly Leu Gln Tyr Ala Ala Lys Phe Ile
232          20          25          30
234 Lys Lys Arg Arg Thr Lys Ser Ser Arg Arg Gly Val Ser Arg Glu Asp
235          35          40          45
237 Ile Glu Arg Glu Val Ser Ile Leu Lys Glu Ile Gln His Pro Asn Val
238   50          55          60
240 Ile Thr Leu His Glu Val Tyr Glu Asn Lys Thr Asp Val Ile Leu Ile
241  65          70          75          80
243 Leu Glu Leu Val Ala Gly Gly Glu Leu Phe Asp Phe Leu Ala Glu Lys
244          85          90          95
246 Glu Ser Leu Thr Glu Glu Glu Ala Thr Glu Phe Leu Lys Gln Ile Leu
247          100         105         110
249 Asn Gly Val Tyr Tyr Leu His Ser Leu Gln Ile Ala His Phe Asp Leu
250          115         120         125
252 Lys Pro Glu Asn Ile Met Leu Leu Asp Arg Asn Val Pro Lys Pro Arg
253          130         135         140
255 Ile Lys Ile Ile Asp Phe Gly Leu Ala His Lys Ile Asp Phe Gly Asn
256 145          150         155         160
258 Glu Phe Lys Asn Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile
259          165         170         175
261 Val Asn Tyr Glu Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly
262          180         185         190
264 Val Ile Thr Tyr Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp
265          195         200         205
267 Thr Lys Gln Glu Thr Leu Ala Asn Val Ser Ala Val Asn Tyr Glu Phe
268          210         215         220
270 Glu Asp Glu Tyr Phe Ser Asn Thr Ser Ala Leu Ala Lys Asp Phe Ile
271 225          230         235         240
273 Arg Arg Leu Leu Val Lys Asp Pro Lys Lys Arg Met Thr Ile Gln Asp
274          245         250         255
276 Ser Leu Gln His Pro Trp Ile
277          260
280 <210> SEQ ID NO: 4
281 <211> LENGTH: 263
282 <212> TYPE: PRT
283 <213> ORGANISM: Human
285 <400> SEQUENCE: 4
286 Tyr Glu Met Gly Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Arg
287   1          5          10          15

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289 Lys Cys Arg Gln Lys Gly Thr Gly Lys Glu Tyr Ala Ala Lys Phe Ile
290          20          25          30
292 Lys Lys Arg Arg Leu Ser Ser Ser Arg Arg Gly Val Ser Arg Glu Glu
293          35          40          45
295 Ile Glu Arg Glu Val Asn Ile Leu Arg Glu Ile Arg His Pro Asn Ile
296          50          55          60
298 Ile Thr Leu His Asp Ile Phe Glu Asn Lys Thr Asp Val Val Leu Ile
299          65          70          75          80
301 Leu Glu Leu Val Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Glu Lys
302          85          90          95
304 Glu Ser Leu Thr Glu Asp Glu Ala Thr Gln Phe Leu Lys Gln Ile Leu
305          100         105         110
307 Asp Gly Val His Tyr Leu His Ser Lys Arg Ile Ala His Phe Asp Leu
308          115         120         125
310 Lys Pro Glu Asn Ile Met Leu Leu Asp Lys Asn Val Pro Asn Pro Arg
311          130         135         140
313 Ile Lys Leu Ile Asp Phe Gly Ile Ala His Lys Ile Glu Ala Gly Asn
314          145         150         155         160
316 Glu Phe Lys Asn Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile
317          165         170         175
319 Val Asn Tyr Glu Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly
320          180         185         190
322 Val Ile Thr Tyr Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Glu
323          195         200         205
325 Thr Lys Gln Glu Thr Leu Thr Asn Ile Ser Ala Val Asn Tyr Asp Phe
326          210         215         220
328 Asp Glu Glu Tyr Phe Ser Asn Thr Ser Glu Leu Ala Lys Asp Phe Ile
329          225         230         235         240
331 Arg Arg Leu Leu Val Lys Asp Pro Lys Arg Arg Met Thr Ile Ala Gln
332          245         250         255
334 Ser Leu Glu His Ser Trp Ile
335          260
338 <210> SEQ ID NO: 5
339 <211> LENGTH: 261
340 <212> TYPE: PRT
341 <213> ORGANISM: Human
343 <400> SEQUENCE: 5
344 Leu Cys Pro Gly Arg Glu Leu Gly Arg Gly Lys Phe Ala Val Val Arg
345          1          5          10          15
347 Lys Cys Ile Lys Lys Asp Ser Gly Lys Glu Phe Ala Ala Lys Phe Met
348          20          25          30
350 Arg Lys Arg Arg Lys Gly Gln Asp Cys Arg Met Glu Ile Ile His Glu
351          35          40          45
353 Ile Ala Val Leu Glu Leu Ala Gln Asp Asn Pro Trp Val Ile Asn Leu
354          50          55          60
356 His Glu Val Tyr Glu Thr Ala Ser Glu Met Ile Leu Val Leu Glu Tyr
357          65          70          75          80
359 Ala Ala Gly Gly Glu Ile Phe Asp Gln Cys Val Ala Asp Arg Glu Glu
360          85          90          95

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VERIFICATION SUMMARY

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